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REMARKS

Applicants have substituted into the present specification a new paper copy Sequence Listing section according to 37 C.F.R. §1.821(c) as new pages 1-4. Furthermore, attached hereto is a 3 1/2" disk containing the "Sequence Listing" in computer readable form in accordance with 37 C.F.R. §1.821(e).

The substitute Sequence Listing corrects typographical/clerical errors in SEQ ID NO:11. The nucleotide at position 6 was changed from "c" to "g", and at position 15 from "g" to "c". The correction to SEQ ID NO:11 is supported by the specification at page 4, line 22, and in claim 12, line 4, and does not present new matter.

Applicants have amended the specification to insert SEQ ID Nos, as supported in the present specification.

The following statement is provided to meet the requirements of 37 C.F.R. §1.825(a) and 1.825(b).

I hereby state, in accordance with 37 C.F.R. §1.825(a), that the amendments included in the substitute sheets of the sequence listing are believed to be supported in the application as filed and that the substitute sheets of the sequence listing are not believed to include new matter.

I hereby further state, in accordance with 37 C.F.R. §1.825(b), that the attached copy of the computer readable form is the same as the attached substitute paper copy of the sequence listing.

Under U.S. rules, each sequence must be classified in <213> as an "Artificial Sequence", a sequence of "Unknown" origin, or a sequence originating in a particular organism, identified by its scientific name.

Neither the rules nor the MPEP clarify the nature of the relationship which must exist between a listed sequence and an organism for that organism to be identified as the origin of the sequence under <213>.

Hence, counsel may choose to identify a listed sequence as associated with a particular organism even though that sequence does not occur in nature by itself in that organism (it may be, e.g., an epitopic fragment of a naturally occurring protein, or a cDNA of a naturally occurring mRNA, or even a substitution mutant of a naturally occurring sequence). Hence, the identification of an organism in <213> should not be construed as an admission that the sequence *per se* occurs in nature in said organism.

Similarly, designation of a sequence as "artificial" should not be construed as a representation that the sequence has no association with any organism. For example, a primer or probe may be designated as "artificial" even though it is necessarily complementary to some target sequence, which may occur in nature. Or an "artificial" sequence may be a substitution mutant of a natural sequence, or a chimera of two or more natural sequences, or a cDNA (i.e., intron-free sequence) corresponding to an intron-containing gene, or otherwise a fragment of a natural sequence.

The Examiner should be able to judge the relationship of the enumerated sequences to natural sequences by giving full consideration to the specification, the art cited therein, any further art cited in an IDS, and the results of his or her sequence search against a database containing known natural sequences.

Attached hereto is a marked-up version of the changes made to the specification and claims by the current amendment. The attached page is captioned "Version with markings to show changes made".

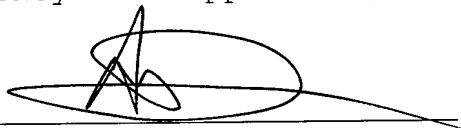
Applicants submit that the present application contains patentable subject matter and therefore urge the examiner to pass the case to issuance.

If the examiner has any questions or comments concerning the above described application, the examiner is urged to contact the undersigned at the phone number below.

Respectfully submitted,

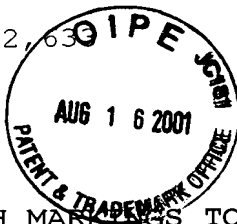
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VERSION WITH MARKINGS TO SHOW CHANGES MADEIn the specification:

The two paragraphs beginning at line 11 of page 3 and ending at line 23 of page 3 have been amended as follows:

(5) The fifth invention is an oligonucleotide characterized in that the gene sequence of a spacer region between a gene coding 16S rRNA and a gene coding 23S rRNA of *Pectinatus frisingensis* has at least one of the following sequence group or the corresponding complementary sequence:

5'-CCATCCTCTTGAAAATCTC-3' ① (SEQ ID NO:5)

5'-TCTCRTCTCACAAGTTTGGC-3' ② (SEQ ID NO:6).

(6) The sixth invention is an oligonucleotide characterized in that the gene sequence of a spacer region between a gene coding 16S rRNA and a gene coding 23S rRNA of *Pectinatus cerevisiiphilus* has at least one of the following sequence group or the corresponding complementary sequence:

5'-CACTCTTACAAGTATCTAC-3' ③ (SEQ ID NO:7)

5'-CCACAATATTTCCGACCAGC-3' ④ (SEQ ID NO:8)

5'-AGTCTTCTCTACTGCCATGC-3' ⑤ (SEQ ID NO:9).

The two paragraphs beginning at line 15 of page 4 and ending at line 22 of page 4 have been amended as follows:

(11) The eleventh invention is a method as in (9), wherein the nucleotide sequence coding the 16S rRNA gene of *Pectinatus frisingensis* has the following sequence:

5'-CGTATCCAGAGATGGATATT-3' ⑥ (SEQ ID NO:10)

(12) The twelfth invention is a method as in (10), wherein the nucleotide sequence coding the 16S rRNA gene of *Pectinatus cerevisiiphilus* has the following sequence:

5'-CGTATGCAGAGATGCATATT-3' ⑦ (SEQ ID NO:11)

In the claims:

Claims 5, 6, 11 and 12 have been amended as follows:

5 (Amended). An oligonucleotide characterized in that the gene sequence of a spacer region between a gene coding 16S rRNA and a gene coding 23S rRNA of *Pectinatus frisingensis* has at least one of the following sequence group or the corresponding complementary sequence:

5'-CCATCCTCTTGAAAATCTC-3' ① (SEQ ID NO:5)

5'-TCTCRTCTCACAAAGTTTGGC-3' ② (SEQ ID NO:6).

6 (Amended). An oligonucleotide characterized in that the gene sequence of a spacer region between a gene coding 16S rRNA and a gene coding 23S rRNA of *Pectinatus cerevisiiphilus* has at least one of the following sequence group or the corresponding complementary sequence:

5'-CACTCTTACAAGTATCTAC-3' ③ (SEQ ID NO:7)

5'-CCACAATATTTCCGACCAGC-3' ④ (SEQ ID NO:8)

5'-AGTCTTCTCTACTGCCATGC-3' ⑤ (SEQ ID NO:9).

11 (Amended). A method as claimed in claim 9, wherein the nucleotide sequence coding the 16S rRNA gene of *Pectinatus frisingensis* has the following sequence:

5'-CGTATCCAGAGATGGATATT-3' ⑥ (SEQ ID NO:10)

12 (Amended). A method as claimed in claim 10,  
wherein the nucleotide sequence coding the 16S rRNA gene of  
*Pectinatus cerevisiiphilus* has the following sequence:

5'-CGTATGCAGAGATGCATATT-3' ⑦ (SEQ ID NO:11)